

Page 1

Query Match	99.6%;	Score 1186.2;	DB 1;	Length 1204
Best Local Similarity	99.7%;	Pred. No. 0;		

10

```
QY 1081 ATCGGGTTAAGCTTTGATTTCTGCTTTCTCATATGAGTGGCGTACATCACTCCG 1140
DB 1088 ATCGGCTTAAGCTTTGATTTCTGCTTTCTCATATGAGTGGCGTACATCACTCCG 1147
QY 1141 ATTGAAAACAGTGTATATACGATTTAAAGAGCTTCGGTGTGAAAATGTAA 1191
DB 1148 ATTGAAAACAGTGTATATACGATTTAAAGAGCTTCGGTGTGAAAATGTAA 1198

RESULT 2
US-09-869-334B-43
; Sequence 43, Application US/09869334B
; GENERAL INFORMATION:
; APPLICANT: ENDO, Hirofumi
; APPLICANT: MIZOGUCHI, Hiroshi
; APPLICANT: OZAKI, Akio
; APPLICANT: YONETANI, Yoshiyuki
; APPLICANT: HASHIMOTO, Shin-ichi
; TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
; FILE REFERENCE: P21289
; CURRENT APPLICATION NUMBER: US/09/869,334B
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT JP00/00472
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-869-334B-43

Query Match 99.2%; Score 1181.4; DB 1; Length 1221;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1185; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAAATGTTTAAACCGCGGCAAGCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAA 60
DB 25 ATGAAATGTTTAAACCGCGGCTGCAAGCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAA 84
QY 61 CAGGATGCTATCATCGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 120
DB 85 CAGGATGCTATCATCGCTTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 144
QY 121 TTTGATGAAGAAACCAAGTGTGAGCGCTTTTCTTATGATGATGATGATGATGATGAT 180
DB 145 TTTGATGAAGAAACCAAGTGTGAGCGCTTTTCTTATGATGATGATGATGATGATGAT 204
QY 181 GGGGATGAAGAGTGTGTTTCCAGTTGCATGCGCAGCAGCAGCAGCTATTGGAATTC 240
DB 205 GGGGATGAAGAGTGTGTTTCCAGTTGCATGCGCAGCAGCAGCAGCTATTGGAATTC 264
QY 241 ATATTTAAATGAGACCCCGGCAAGCTTAACAAAATCCCTTCGTGTGTAACAAACCTTT 300
DB 265 ATATTTAAATGAGACCCCGGCAAGCTTAACAAAATCCCTTCGTGTGTAACAAACCTTT 324
QY 301 ACTCCGCGGTGATGAAGCAATGGAACCGAGATTCAGAAATCAAGATGAATGAT 360
DB 325 ACTCCGCGGTGATGAAGCAATGGAACCGAGATTCAGAAATCAAGATGAATGAT 384
QY 361 CAAAAATTTGAGGGGCGCAGTGAAGTTTGAACCTTTTCACGATTTTCAATCCCGCTTCG 420
DB 385 CAAAAATTTGAGGGGCGCAGTGAAGTTTGAACCTTTTCACGATTTTCAATCCCGCTTCG 444
QY 421 GTATTTGATGATCTGAGCTGCTGAGAGTGCCTTTCAGCCGAGATGGAACAGTTTAAAGCA 480
DB 445 GTATTTGATGATCTGAGCTGCTGAGAGTGCCTTTCAGCCGAGATGGAACAGTTTAAAGCA 504
QY 481 TGGTCTGATCTTTTGGTCACTACACCGAAGATTAAGTAAGTAAGTAAGTAAGTAAGTAAG 540
DB 505 TGGTCTGATCTTTTGGTCACTACACCGAAGATTAAGTAAGTAAGTAAGTAAGTAAGTAAG 564
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QY 541 TTGAAAGAACGAGATTAAGTGTGAGAGAACTGCGCGCTTTTTCGCGCATCATAGA 600
DB 565 TTGAAAGAACGAGATTAAGTGTGAGAGAACTGCGCGCTTTTTCGCGCATCATAGA 624
QY 601 GAAAGCGAAACCAACCGGAAACAGATATTATTTCATTTTGTGGAACGGAAGAAACA 660
DB 625 GAAAGCGAAACCAACCGGAAACAGATATTATTTCATTTTGTGGAACGGAAGAAACA 684
QY 661 GGGGAGAGCTGTCCGCTGAGAGCTGATTCGCTTTTGGACGCTGCTGTGTGTCGGA 720
DB 685 GGGGAGAGCTGTCCGCTGAGAGCTGATTCGCTTTTGGACGCTGCTGTGTGTCGGA 744
QY 721 AATGAAACCACTACAACTGATTTTAAATGCGATGTAACGATATTAAACGCGAGGC 780
DB 745 AATGAAACCACTACAACTGATTTTAAATGCGATGTAACGATATTAAACGCGAGGC 804
QY 781 GTTTACGAGAACTGCGCAGCCATCCTGAATGATGCTCAGGCACTGAGAGAGCCTTG 840
DB 805 GTTTACGAGAACTGCGCAGCCATCCTGAATGATGCTCAGGCACTGAGAGAGCCTTG 864
QY 841 CGTTTCAAGCGCGCGCCCGCTTTTGAAGCGCATTTGCCAAGCGGATACGAGATCGGG 900
DB 865 CGTTTCAAGCGCGCGCCCGCTTTTGAAGCGCATTTGCCAAGCGGATACGAGATCGGG 924
QY 901 GGGGACCTGATTAAGAGAGTGAATGATTTTGGCGTTTGTGGCATCGCAAAATCGTAT 960
DB 925 GGGGACCTGATTAAGAGAGTGAATGATTTTGGCGTTTGTGGCATCGCAAAATCGTAT 984
QY 961 GAAGCAAAAGTTTGAACAGCCGACATGTTGATATCCGCGCCATCCGATTCGATATT 1020
DB 985 GAAGCAAAAGTTTGAACAGCCGACATGTTGATATCCGCGCCATCCGATTCGATATT 1044
QY 1021 GCGTTTGGCAGCGCATCCATTTTTCGCTTGGGCGCCCGCTTCCCGCTTGAAGCAAT 1080
DB 1045 GCGTTTGGCAGCGCATCCATTTTTCGCTTGGGCGCCCGCTTCCCGCTTGAAGCAAT 1104
QY 1081 ATCGGTTAAAGCTTTGATTTTCTGCTTTTCTCATATGAGTGGCGTACATCACTCCG 1140
DB 1105 ATCGGTTAAAGCTTTGATTTTCTGCTTTTCTCATATGAGTGGCGTACATCACTCCG 1164
QY 1141 ATTGAAAACAGTGTATATACGATTTAAAGAGCTTCGGTGTGAAAATGTAA 1191
DB 1165 ATTGAAAACAGTGTATATACGATTTAAAGAGCTTCGGTGTGAAAATGTAA 1215

RESULT 3
US-09-869-334B-44
; Sequence 44, Application US/09869334B
; GENERAL INFORMATION:
; APPLICANT: ENDO, Hirofumi
; APPLICANT: MIZOGUCHI, Hiroshi
; APPLICANT: OZAKI, Akio
; APPLICANT: YONETANI, Yoshiyuki
; APPLICANT: HASHIMOTO, Shin-ichi
; TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
; FILE REFERENCE: P21289
; CURRENT APPLICATION NUMBER: US/09/869,334B
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: PCT JP00/00472
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 1221
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-869-334B-44

Query Match 98.1%; Score 1168.6; DB 1; Length 1221;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1177; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGAAATGTTTAAACCGCGGCAAGCTTGCAGCGAGCGCTGCTCAATGGGAAAAACAA 60
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Db 25 ATGAACTGTTGAAACCGCCGTCAGGCTTCCGCGACCGCTGCTCAATGGGAAAAACAA 84

QY 61 CAGGATGGCGATCAATCCGCTTCCATGGTATGAATCCATGAAAGATGGCGCTGTTCC 120

Dd 85 CAGGATGGCGATCAATCCGCTTCCATGGTATGAATCGATGAAAGATGGCGCTGTTCC 144

QY 121 TTTCATGAGAAACCAAGTGTGGAGCGCTTTTCTTATATGATGTCAAAAAAGTTGT 180

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Db      1105 ATCCGCTTAAAGCTTTGATTTCGCTTTTCCTCATAGAGTGCAGTCACTCCG 1164
Qy      1141 ATTTAAAAACAATGATATTAACGATTTAAAGAGCTCCGTCGGAATAATGTAA 1191
Db      1165 ATTGAAACCACTGTGATTAACGATTAAAGAGCTTCCTGTGGAATGTAA 1215

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Search completed: March 31, 2004, 08:15:34
JOD time : 3 secs

QY	181	GGGGAATAAGAGTGTGTTTCCAGTGGATGATCCGACAGACGACAGCTCTATTGGAAATTC	240
Db	205	GGGGATTAAGAGTGTGTTTCCAGTGGATGATCCGACAGACGACAGCTCTATTGGAAATTC	264
QY	241	ATCATTAAACATGAGACCCGCGGAAGCATCAAAAATCCGTTCACTCGTGAACAAAGCCTTT	300
Db	265	ATCATTAGCATGAGACCCGCGGAAGCATCAAAAATCCGTTCACTCGTGAACAAAGCCTTT	324
QY	301	ACTGCCGCGCATGAGACATGGAGAACCGAGATTCAAGAAATCAGATGAACTGATT	360
Db	325	ACTGCCGCGCGATGAGACATGGAGAACCGAGATTCAAGAAATCAGATGAACTGATT	384
QY	361	CAAAAATTTGAGGGGCGCAGTGAAGTTGACCTTGTTCACATTTTTCATACCCGCTTCG	420
Db	385	CAAAAATTTGAGGGGCGCAGTGAAGTTGACCTTGTTCACATTTTTCATACCCGCTTCG	444
QY	421	GTTATTGTGATATGTAGCTGCTGGAGATGCTTCAACGAGATGGAACAGTTTAAAGCA	480
Db	445	GTTATTGTGATATGTAGCTGCTGGAGATGCTTCAACGAGATGGAACAGTTTAAAGCA	504
QY	481	TGCTCTGATCTTCTGCTCAGTACACCGAAGATPAAAGTGAAGAAGCTGAAAAAGCTTT	540
Db	505	TGCTCTGATCTTCTGCTCAGTACACCGAAGATPAAAGTGAAGAAGCTGAAAAAGCTTT	564
QY	541	TTGGAAGAACAGATTAAGTGTGAGAGAAATGTGGCCGCGTTTGTGCGGATCATGAA	600
Db	565	TTGGAAGAACAGATTAAGTGTGAGAGAAATGTGGCCGCGTTTGTGCGGATCATGAA	624
QY	601	GAAAAGCAAAACAACCGGAACAGGATATTATTCTATTATTAGTGAAGCGGAAGAAACA	660
Db	625	GAAAAGCAAAACAACCGGAACAGGATATTATTCTATTATTAGTGAAGCGGAAGAAACA	684
QY	661	GGCGAAGAGCTGTCCGCTGGAAGAGCTGATTCGCCGTTTGACAGCGTGTGCTGGGCGGA	720
Db	685	GGCGAAGAGCTGTCCGCTGGAAGAGCTGATTCGCCGTTTGACAGCGTGTGCTGGGCGGA	744
QY	721	AATGAACCATCAACAACTGATTTCAATCGATGTAACACATATTGAACCGCACGC	780
Db	745	AATGAACCATCAACAACTGATTTCAATCGATGTAACACATATTGAACCGCACGC	804
QY	781	GTTTTCGAGGAATCTGCGCAGCATCTCTGAATCTGATGCTCAGGAGTGGAGAGGCGCTG	840
Db	805	GTTTTCGAGGAATCTGCGCAGCATCTCTGAATCTGATGCTCAGGAGTGGAGAGGCGCTG	864
QY	841	CGTTTCAGAGCGCCGGCCCGGTTTGAAGGCGCATTTGCCAAGCGGGATACGAGATCGGG	900
Db	865	CGTTTCAGAGCGCCGGCCCGGTTTGAAGGCGCATTTGCCAAGCGGGATACGAGATCGGG	924
QY	901	GGGCACTCGATTAAAGAGTGTATGTGTTTGGCGTTTGTGGCATCGGCAAAATCGGAT	960
Db	925	GGGCACTCGATTAAAGAGTGTATGTGTTTGGCGTTTGTGGCATCGGCAAAATCGGAT	984
QY	961	GAAAGCAAGTTGACAGACCGCACATGTTTGATATCCGCGCGCATCCCAATCCGCATATT	1020
Db	985	GAAAGCAAGTTGACAGACCGCACATGTTTGATATCCGCGCGCATCCCAATCCGCATATT	1044
QY	1021	GCGTTTGGCCACGCGCATTCATTTTGTGCTTGGGGCCCGGCTTGCCCGCTTGAAGCAAT	1080
Db	1045	GCGTTTGGCCACGCGCATTCATTTTGTGCTTGGGGCCCGGCTTGCCCGCTTGAAGCAAT	1104
QY	1081	ATCGGCTTAAGCTCTTGTGATTTCTGCTTTTCTCATATGAGTGTGCTAGATVCACTCG	1140

Wed Mar 31 08:15:56 2004

align1

Page 1

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OM protein - protein search, using sw model

Run on: March 31, 2004, 08:11:35 ; Search time 0.001 Seconds
(without alignments)
313.632 Million cell updates/sec

Title: us-09-869-334b-1

Sequence: 1 MNVLRQALORALNGKKNK.....STPIENSVYGLKSRVYM 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 792 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database: us-09-869-334b-4:*
1: /home/sdavid/david-cmp/marc04/ramirez334/us-09-869-334b-42:*
2: /home/sdavid/david-cmp/marc04/ramirez334/us-09-869-334b-45:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	99.5	396	1 us-09-869-334b-42	
2	2018	98.3	396	2 us-09-869-334b-45	

ALIGNMENTS

RESULT 1
us-09-869-334b-42

Query Match 99.5%; Score 2042; DB 1; Length 396;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MNVLRQALORALNGKKNKODAYHPFPWYSEMRKDAVVSFDEENQVSVFLYDVKKV 60

1 MNVLRQALORALNGKKNKODAYHPFPWYSEMRKDAVVSFDEENQVSVFLYDVKKV 60

61 GDXELFSSCMPQOTSSIGNSIINMDPPYHTKIRSVNKAFTPRVWKQWEPRIOETIDELI 120

61 GDXELFSSCMPQOTSSIGNSIINMDPPYHTKIRSVNKAFTPRVWKQWEPRIOETIDELI 120

121 QKFGSRSEPDVHDSYPLPVIVISELGVSAHMEQFKASDILVSTPKDSEAEKAF 180

121 QKFGSRSEPDVHDSYPLPVIVISELGVSAHMEQFKASDILVSTPKDSEAEKAF 180

181 LEERDKCEBELAFAFAGIIEEKRNKPEODIISILVEAETGKLSGSELLIPCTLLLVAG 240

181 LEERDKCEBELAFAFAGIIEEKRNKPEODIISILVEAETGKLSGSELLIPCTLLLVAG 240

241 NETTNLISNANYSILETPGVYEELRSHBELMPQAVEALRRAPAPVLRRIAKRDEIG 300

Search completed: March 31, 2004, 08:11:36
Job time: 1 sec

RESULT 2
us-09-869-334b-45

Query Match 98.3%; Score 2018; DB 2; Length 396;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 389; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MNVLRQALORALNGKKNKODAYHPFPWYSEMRKDAVVSFDEENQVSVFLYDVKKV 60

1 MNVLRQALORALNGKKNKODAYHPFPWYSEMRKDAVVSFDEENQVSVFLYDVKKV 60

61 GDXELFSSCMPQOTSSIGNSIINMDPPYHTKIRSVNKAFTPRVWKQWEPRIOETIDELI 120

61 GDXELFSSCMPQOTSSIGNSIINMDPPYHTKIRSVNKAFTPRVWKQWEPRIOETIDELI 120

121 QKFGSRSEPDVHDSYPLPVIVISELGVSAHMEQFKASDILVSTPKDSEAEKAF 180

121 QKFGSRSEPDVHDSYPLPVIVISELGVSAHMEQFKASDILVSTPKDSEAEKAF 180

181 LEERDKCEBELAFAFAGIIEEKRNKPEODIISILVEAETGKLSGSELLIPCTLLLVAG 240

181 LEERDKCEBELAFAFAGIIEEKRNKPEODIISILVEAETGKLSGSELLIPCTLLLVAG 240

241 NETTNLISNANYSILETPGVYEELRSHBELMPQAVEALRRAPAPVLRRIAKRDEIG 300

241 NETTNLISNANYSILETPGVYEELRSHBELMPQAVEALRRAPAPVLRRIAKRDEIG 300

301 GHLIKGDMVLAFAVASANRDEAKFDRPHMFDIRRHPPHIAFGHIFCLGAPLARLEAN 360

301 GHLIKGDMVLAFAVASANRDEAKFDRPHMFDIRRHPPHIAFGHIFCLGAPLARLEAN 360

361 IALTSLISAFPHMECVSITPIENSVYGLKSRVYM 396

361 IALTSLISAFPHMECVSITPIENSVYGLKSRVYM 396

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OM protein - protein search, using SW model

Run on: March 31, 2004, 08:08:52 ; Search time 0.001 Seconds
(without alignments)
470.448 Million cell updates/sec

Title: 2633575

Sequence: 1 mrvlnrrqalqralngknk.....stlepiensviyglksfrvkm 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3 segs, 1188 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database : US09869334B.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2052	100.0	396	1	US-09-869-334B-1
2	2042	99.5	396	1	US-09-869-334B-42
3	2018	98.3	396	1	US-09-869-334B-45

ALIGNMENTS

RESULT 1
US-09-869-334B-1

Sequence 1, Application US/09869334B
GENERAL INFORMATION:
APPLICANT: ENDO, Hirofumi
APPLICANT: MIZOGUCHI, Hiroshi
APPLICANT: OZAKI, Akio
APPLICANT: YONETANI, Yoshiyuki
APPLICANT: HASHIMOTO, Shin-ichi
TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
FILE REFERENCE: P21289
CURRENT APPLICATION NUMBER: US/09/869,334B
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: PCT JP00/00472
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 1
LENGTH: 396
TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-869-334B-1

Query Match 100.0%; Score 2052; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MMVLRNRRQALQRALNGKNKQDAVHPFPMYESMRKDAVSPDEENQVMSVFLYDDVKVY	60
DB	1	MMVLRNRRQALQRALNGKNKQDAVHPFPMYESMRKDAVSPDEENQVMSVFLYDDVKVY	60
QY	61	GDKELFSSCMPOOTSISINSIIMDPKTKIRSVNKAFTPRVWKQMEPRIQETIDELI	120
DB	61	GDKELFSSCMPOOTSISINSIIMDPKTKIRSVNKAFTPRVWKQMEPRIQETIDELI	120
QY	121	QKFGRSSEFDLVHDSFYPVIVISSELLGVPSAHNEQFKVMSDLLVSTPKXSEBAEKAF	180
DB	121	QKFGRSSEFDLVHDSFYPVIVISSELLGVPSAHNEQFKVMSDLLVSTPKXSEBAEKAF	180
QY	181	LEERDKCEBELAFAFGIIEERKNPEODIISILVEAETGKSGEELIPCTILLVAG	240
DB	181	LEERDKCEBELAFAFGIIEERKNPEODIISILVEAETGKSGEELIPCTILLVAG	240
QY	241	NETTNLSNAMYSLFETPGVYEEBRSHELMPOAVEELRFRAPVLRRIAKDTEIG	300
DB	241	NETTNLSNAMYSLFETPGVYEEBRSHELMPOAVEELRFRAPVLRRIAKDTEIG	300
QY	301	GHILKEGDMVLAFAVANSRDEAKFDRPMFDIRRHNPVHIAFGHIFCLGAPLARLEAN	360
DB	301	GHILKEGDMVLAFAVANSRDEAKFDRPMFDIRRHNPVHIAFGHIFCLGAPLARLEAN	360
QY	361	IALTSLISAFPMHECVSITPIENSVTYGLKSPRVKM	396
DB	361	IALTSLISAFPMHECVSITPIENSVTYGLKSPRVKM	396

RESULT 2
US-09-869-334B-42

Sequence 42, Application US/09869334B
GENERAL INFORMATION:
APPLICANT: ENDO, Hirofumi
APPLICANT: MIZOGUCHI, Hiroshi
APPLICANT: OZAKI, Akio
APPLICANT: YONETANI, Yoshiyuki
APPLICANT: HASHIMOTO, Shin-ichi
TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
FILE REFERENCE: P21289
CURRENT APPLICATION NUMBER: US/09/869,334B
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: PCT JP00/00472
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 42
LENGTH: 396
TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-869-334B-42

Query Match 99.5%; Score 2042; DB 1; Length 396;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MMVLRNRRQALQRALNGKNKQDAVHPFPMYESMRKDAVSPDEENQVMSVFLYDDVKVY	60
DB	1	MMVLRNRRQALQRALNGKNKQDAVHPFPMYESMRKDAVSPDEENQVMSVFLYDDVKVY	60
QY	61	GDKELFSSCMPOOTSISINSIIMDPKTKIRSVNKAFTPRVWKQMEPRIQETIDELI	120
DB	61	GDKELFSSCMPOOTSISINSIIMDPKTKIRSVNKAFTPRVWKQMEPRIQETIDELI	120
QY	121	QKFGRSSEFDLVHDSFYPVIVISSELLGVPSAHNEQFKVMSDLLVSTPKXSEBAEKAF	180
DB	121	QKFGRSSEFDLVHDSFYPVIVISSELLGVPSAHNEQFKVMSDLLVSTPKXSEBAEKAF	180
QY	181	LEERDKCEBELAFAFGIIEERKNPEODIISILVEAETGKSGEELIPCTILLVAG	240
DB	181	LEERDKCEBELAFAFGIIEERKNPEODIISILVEAETGKSGEELIPCTILLVAG	240

Qy	241	NETTTMLISAMYSIIETGVVEELRSHHELMPOVEALFPAPAPULRIARDDEIG	300
Db	241	NETTTMLISAMYSIIETGVVEELRSHHELMPOVEALFPAPAPULRIARDDEIG	300
Qy	301	GHIIEKGDWLVAVASANDRAKPRBPMPFDIRRPNEHIAFGHIGHCGLAPLARLEAN	360
Db	301	GHIIEKGDWLVAVASANDRAKPRBPMPFDIRRPNEHIAFGHIGHCGLAPLARLEAN	360
Qy	361	IALTSLISAFPHECVSITPIENSIVYGLKSRVVM	396
Db	361	IALTSLISAFPHECVSITPIENSIVYGLKSRVVM	396

RESULT 3

US-09-869-334B-45
Sequence 45, Application US/09869334B
GENERAL INFORMATION:
APPLICANT: ENDO, Hirofumi
APPLICANT: MIZOGUCHI, Hiroshi
APPLICANT: OZAKI, Akio
APPLICANT: YONETANI, Yoshiyuki
APPLICANT: HASHIMOTO, Shiro-ichi
TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor
FILE REFERENCE: P21289
CURRENT APPLICATION NUMBER: US/09/869,334B
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: PCT JP00/00472
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
SEQ ID NO 45
LENGTH: 396
TYPE: PR1
ORGANISM: Bacillus subtilis
US-09-869-334B-45

Query Match	98.3%	Score 2018;	DB 1;	length 396;
Best Local Similarity	96.2%	Pred. No. 0;		
Matches 389;	Conservative	3;	Mismatches 4;	Indels 0;
				Gaps 0;

QY	I	MVTLNRRQALQRLLLNGKNKODAYHFPFMYESMRKODAVSDENQWVSFTLDDVQKV	60
Db	1	MVTLNRRQALPRLLINGKNKODAYHFPFMYESMRKODAVSDENQWVSFLDDVQKV	60
QY	61	GDKELFSSCMPQOOTSSIGNSIIMDDPKTKTKRSVYNKAFTPRVKQWEPRIQETDELT	120
Db	61	GDKELFSSCMPQOOTSSIGNSIIMDDPKTKTKRSVYNKAFTPRKMQWEPRIQETDELT	120
QY	121	QKFGGRSEFDLVHDVSYPLFVIVISELLGVPSAHNEQFKASDILLVSTPRKXSEAEKAF	180
Db	121	QKFGGRSEFDLVHDVSYPLFVIVISELLGVPSAHNEQFKASDILLVSTPRKXSEAEKAF	180
QY	181	LEEDKCKEEBELAAFPACITIEKKNKREBOITISLYBAETGKLSGELLPLCTLLLVAG	240
Db	181	LEEDKCKEEBELAAFPACITIEKKNKREBOITISLYBAETGKLSGELLPLCTLLLVAG	240
QY	241	NETTNTNISNAMSITETPGVYEELSHPELMPQAVEELRPRAPAPVLRIRAKRDEIG	300
Db	241	NETTNTNISNAMSITETPGVYEELSHPELMPQAVEELRPRAPAPVLRIRAKRDEIG	300
QY	361	GHLIKEGDMVLAFAVASANRDEAKFDRPHMFDIRHNPRIAGHGIMFCGLAPLARLEAN	360
Db	361	GHLIKEGDMVLAFAVASANRDEAKFDRPHMFDIRHNPRIAGHGIMFCGLAPLARLEAN	360
QY	361	IATLSLISAPPHMECVSITPIENSIVYGLKSRFVKK	396
Db	361	IATLSLISAPPHMECVSITPIENSIVYGLKSRFVKK	396

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2004, 08:08:52 ; Search time 0.001 Seconds
(without alignments)

470.448 Million cell updates/sec

Title: 2633575
Perfect score: 2052
Sequence: 1 mvtlnrrqalqralnknk.....stlplensviyglksfrvkm 396

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 3 seqs, 1188 residues

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 3 summaries

Database: US09869334B.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2052	100.0	396	1 US-09-869-334B-1	Sequence 1, Appl1
2	2042	99.5	396	1 US-09-869-334B-42	Sequence 42, Appl1
3	2018	98.3	396	1 US-09-869-334B-45	Sequence 45, Appl1

ALIGNMENTS

RESULT 1

US-09-869-334B-1

Sequence 1, Application US/09869334B

GENERAL INFORMATION:

APPLICANT: ENDO, Hirofumi

APPLICANT: MIZOGUCHI, Hiroshi

APPLICANT: OZAKI, Akio

APPLICANT: YONETANI, Yoshiyuki

APPLICANT: HASHIMOTO, Shin-ichi

TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor

FILE REFERENCE: P21289

CURRENT APPLICATION NUMBER: US/09/869, 334B

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: PCT JP00/00472

PRIOR FILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1

LENGTH: 396

TYPE: PRT

ORGANISM: Bacillus subtilis

US-09-869-334B-1

Query Match 100.0%; Score 2052; DB 1; Length 396;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVTLNRRQALQRALNKNKQDAVHPFPMYESNRKQAPVAFDEENQVMSVFLYDDVKVY	60
DB	1	MVTLNRRQALQRALNKNKQDAVHPFPMYESNRKQAPVAFDEENQVMSVFLYDDVKVY	60
QY	61	GDKELFSSCMPQOTSIGNSIINMDPKTKIRSVVNKATTPRMKQWEPRIOITDELI	120
DB	61	GDKELFSSCMPQOTSIGNSIINMDPKTKIRSVVNKATTPRMKQWEPRIOITDELI	120
QY	121	QKFGRSFEDLVHDSYPLPVIVISELLGVPSAHMEQFAMSDLVSTPKDSEAEKAF	180
DB	121	QKFGRSFEDLVHDSYPLPVIVISELLGVPSAHMEQFAMSDLVSTPKDSEAEKAF	180
QY	181	LEERDKCEELAAFPAGIIEERKNRPEODIISILVEAEFGKLSGELLIPCTLLIVAG	240
DB	181	LEERDKCEELAAFPAGIIEERKNRPEODIISILVEAEFGKLSGELLIPCTLLIVAG	240
QY	241	NETTNLISNMYGILTEPGVYEEELRSHPELMPQAVEALRFRAPVLRIRARDEIG	300
DB	241	NETTNLISNMYGILTEPGVYEEELRSHPELMPQAVEALRFRAPVLRIRARDEIG	300
QY	301	GHILKEGDMVLAFAVASANRDEAKFDRPHMEDIRRHPRPHIAFGHIGCLGAPLARLEAN	360
DB	301	GHILKEGDMVLAFAVASANRDEAKFDRPHMEDIRRHPRPHIAFGHIGCLGAPLARLEAN	360
QY	361	IATLSLISAPPHMGCVSTIPIENSVIYGLKSFYKX	396
DB	361	IATLSLISAPPHMGCVSTIPIENSVIYGLKSFYKX	396

RESULT 2

US-09-869-334B-42

Sequence 42, Application US/09869334B

GENERAL INFORMATION:

APPLICANT: ENDO, Hirofumi

APPLICANT: MIZOGUCHI, Hiroshi

APPLICANT: OZAKI, Akio

APPLICANT: YONETANI, Yoshiyuki

APPLICANT: HASHIMOTO, Shin-ichi

TITLE OF INVENTION: Process for Producing HMG-CoA Reductase Inhibitor

FILE REFERENCE: P21289

CURRENT APPLICATION NUMBER: US/09/869, 334B

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: PCT JP00/00472

PRIOR FILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn version 3.2

SEQ ID NO 42

LENGTH: 396

TYPE: PRT

ORGANISM: Bacillus subtilis

US-09-869-334B-42

Query Match 99.5%; Score 2042; DB 1; Length 396;
Best Local Similarity 99.5%; Pred. No. 0;

Matches 394; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	MVTLNRRQALQRALNKNKQDAVHPFPMYESNRKQAPVAFDEENQVMSVFLYDDVKVY	60
DB	1	MVTLNRRQALQRALNKNKQDAVHPFPMYESNRKQAPVAFDEENQVMSVFLYDDVKVY	60
QY	61	GDKELFSSCMPQOTSIGNSIINMDPKTKIRSVVNKATTPRMKQWEPRIOITDELI	120
DB	61	GDKELFSSCMPQOTSIGNSIINMDPKTKIRSVVNKATTPRMKQWEPRIOITDELI	120
QY	121	QKFGRSFEDLVHDSYPLPVIVISELLGVPSAHMEQFAMSDLVSTPKDSEAEKAF	180
DB	121	QKFGRSFEDLVHDSYPLPVIVISELLGVPSAHMEQFAMSDLVSTPKDSEAEKAF	180
QY	181	LEERDKCEELAAFPAGIIEERKNRPEODIISILVEAEFGKLSGELLIPCTLLIVAG	240
DB	181	LEERDKCEELAAFPAGIIEERKNRPEODIISILVEAEFGKLSGELLIPCTLLIVAG	240